

# SEQUENCE LISTING

<110> YOSHIMURA, Koji  
HIKICHI, Yuichi  
NISHIMURA, Atsushi

<120> Novel Protein and DNA Thereof

<130> 2544 US1N

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<150> US 09/786256

<151> 2001-03-02

<150> PCT/JP99/04766

<151> 1999-09-02

<150> JP 10-250115

<151> 1998-09-03

<160> 32

<170> PatentIn version 3.0

<210> 1

<211> 540

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(540)

<223> An isolated ADAM family protein

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Pro	Ile	Arg	Leu	His	Pro	Leu	His	Lys	Arg	Glu	Ala	Lys	Glu	Pro	Glu
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Gln	Gln	Glu	Gln	Phe	Glu	Thr	Glu	Leu	Lys	Tyr	Lys	Met	Thr	Ile	Asn
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Gly	Lys	Ile	Ala	Val	Leu	Tyr	Leu	Lys	Lys	Asn	Lys	Asn	Leu	Leu	Ala
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Pro	Gly	Tyr	Thr	Glu	Thr	Tyr	Tyr	Asn	Ser	Thr	Gly	Lys	Glu	Ile	Thr
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Thr	Ser	Pro	Gln	Ile	Met	Asp	Asp	Cys	Tyr	Tyr	Gln	Gly	His	Ile	Leu
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Asn	Glu	Lys	Val	Ser	Asp	Ala	Ser	Ile	Ser	Thr	Cys	Arg	Gly	Leu	Arg	
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Tyr	Leu	Val	Leu	Asp	Asn	Gly	Glu	Phe	Lys	Arg	Tyr	Asn	Glu	Asn	Gln	
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Asp	Glu	Ile	Arg	Lys	Arg	Val	Phe	Glu	Met	Ala	Asn	Tyr	Val	Asn	Met	
225					230					235					240	
Leu	Tyr	Lys	Lys	Leu	Asn	Thr	His	Val	Ala	Leu	Val	Gly	Met	Glu	Ile	
245					250					255						
Trp	Thr	Asp	Lys	Asp	Lys	Ile	Lys	Ile	Thr	Pro	Asn	Ala	Ser	Phe	Thr	
260					265					270						
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275					280					285						
Arg	His	Asp	Ile	Ala	Gln	Leu	Ile	Thr	Ala	Thr	Glu	Leu	Ala	Gly	Thr	
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Thr	Val	Gly	Leu	Ala	Phe	Met	Ser	Thr	Met	Cys	Ser	Pro	Tyr	Ser	Val	
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Gly	Val	Val	Gln	Asp	His	Ser	Asp	Asn	Leu	Leu	Arg	Val	Ala	Gly	Thr	
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Ser	Cys	Lys	Cys	Pro	Ser	Thr	Ile	Cys	Val	Met	Asp	Lys	Ala	Leu	Ser	
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Phe	Tyr	Ile	Pro	Thr	Asp	Phe	Ser	Ser	Cys	Ser	Arg	Leu	Ser	Tyr	Asp	
370					375					380						
Lys	Phe	Phe	Glu	Asp	Lys	Leu	Ser	Asn	Cys	Leu	Phe	Asn	Ala	Pro	Leu	
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Pro	Thr	Asp	Ile	Ile	Ser	Thr	Pro	Ile	Cys	Gly	Asn	Gln	Leu	Val	Glu	

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			420					425					430		
Cys	Cys	Asp	Ala	Lys	Thr	Cys	Lys	Ile	Lys	Ala	Thr	Phe	Gln	Cys	Ala
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Leu	Gly	Glu	Cys	Cys	Glu	Lys	Cys	Gln	Phe	Lys	Lys	Ala	Gly	Met	Val
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Cys	Arg	Pro	Ala	Lys	Asp	Glu	Cys	Asp	Leu	Pro	Glu	Met	Cys	Asn	Gly
465					470				475						480
Lys	Ser	Gly	Asn	Cys	Pro	Asp	Asp	Arg	Phe	Gln	Val	Asn	Gly	Phe	Pro
				485				490						495	
Cys	His	His	Gly	Lys	Gly	His	Cys	Leu	Met	Gly	Thr	Cys	Pro	Thr	Leu
			500					505					510		
Gln	Glu	Gln	Cys	Thr	Glu	Leu	Trp	Gly	Pro	Gly	Arg	Arg	Thr	Asn	Pro
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 <223> Isolated fragment of Protein of Seq ID No.1 (aa 400-495)

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			20					25					30		
Ile	Cys	Cys	Asp	Ala	Lys	Thr	Cys	Lys	Ile	Lys	Ala	Thr	Phe	Gln	Cys
		35					40					45			
Ala	Leu	Gly	Glu	Cys	Cys	Glu	Lys	Cys	Gln	Phe	Lys	Lys	Ala	Gly	Met
	50					55					60				
Val	Cys	Arg	Pro	Ala	Lys	Asp	Glu	Cys	Asp	Leu	Pro	Glu	Met	Cys	Asn
65					70					75					80
Gly	Lys	Ser	Gly	Asn	Cys	Pro	Asp	Asp	Arg	Phe	Gln	Val	Asn	Gly	Phe
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 <220>  
 <221> misc\_feature  
 <222> (1)..(1620)  
 <223> Isolated DNA encoding for the protein of SEQ ID NO.1

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 gaactccctg .gggtgaagaa gtatgaagtg gtttatccta taagacttca tccactgcat 120  
 aaaagagagg ccaaagagcc agagcaacag gaacaatttg aaactgaatt aaagtataaa 180  
 atgacaatta atggaaaaat tgcagtgcctt tatttgaaaa aaaacaagaa cctccttgca 240  
 ccaggctaca cggaacata ttataattcc actggaaagg agatcaccac aagcccacaa 300  
 attatggatg attgttatta tcaaggacat attcttaatg aaaagggttc tgacgctagc 360  
 atcagcacat gtaggggtct aaggggctac ttcagtcagg gggatcaaag atactttatt 420  
 gaacctttaa gcccataca tcgggatgga caggagcatg cactcttcaa gtataaccct 480  
 gatgaaaaga attatgacag cacctgtggg atggatgggtg tgttggtgggc ccacgatttg 540  
 cagcagaaca ttgccctacc tgccaccaa ctagtaaaat tgaaagacag gaagggttcag 600  
 gaacatgaga aatacataga atattatttg gtcctggata atgggtgagtt taaaagggtac 660  
 aatgagaatc aagatgagat cagaaagagg gtatttgaga tggctaatta tgtcaacatg 720  
 ctttataaaa agctcaatac tcatgtggcc ttagttggta tggaaatctg gactgacaag 780  
 gataagataa agataacccc aaatgcaagc ttcaccttgg agaatttttc taaatggagg 840  
 gggagtgttc tctcaagaag aaagcgtcat gatattgtctc agttaatcac agcaacagaa 900  
 cttgctggaa cgactgtggg tcttgcatth atgtctacaa tgtgttctcc ttattctgtt 960  
 ggcgttggtc aggaccacag cgataatctt cttagagttg cagggacaat ggcacatgaa 1020  
 atgggccaca actttggaat gtttcatgac gactattctt gcaagtgtcc ttctacaata 1080  
 tgtgtgatgg acaaagcact gagcttctat ataccacag acttcagttc ctgcagccgt 1140  
 ctgagctatg acaagttttt tgaagataaa ttatcaaatt gcctctttaa tgctccattg 1200  
 cctacagata tcatatccac tccaatttgt gggaaccagt tgggtggaaat gggagaggac 1260  
 tgtgattgtg ggacatctga ggaatgtacc aatatttgct gtgatgctaa gacatgtaaa 1320  
 atcaaagcaa cttttcaatg tgcattagga gaatgttgtg aaaaatgcca atttaaaaaag 1380

gctgggatgg tgtgcagacc agcaaaagat gagtgcgacc tgcctgaaat gtgtaatggg 1440  
 aaatctggta attgtcctga tgatagattc caagtcaatg gcttcccttg ccatcacggg 1500  
 aagggccact gcttgatggg gacatgcccc aactgcagg agcagtgcac agagctgtgg 1560  
 ggaccaggta ggaggacaaa tcctttcccc tgtgcatgtg cgaaggaaaa tcatttcaga 1620

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 <213> Homo sapiens  
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 <221> misc\_feature  
 <222> (1)..(288)  
 <223> Artificial DNA encoding for peptide of SEQ ID NO.2

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 gactgtgatt gtgggacatc tgaggaatgt accaatattt gctgtgatgc taagacatgt 120  
 aaaatcaaag caacttttca atgtgcatta ggagaatgtt gtgaaaaatg ccaattttaa 180  
 aaggctggga tgggtgtgcag accagcaaaa gatgagtgcg acctgcctga aatgtgtaat 240  
 ggtaaactctg gtaattgtcc tgatgataga ttccaagtca atggcttc 288

<210> 5  
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 <223> Isolated fragment of protein of SEQ ID NO.1 (aa 199-399)

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 1 5 10 15  
 Gly Glu Phe Lys Arg Tyr Asn Glu Asn Gln Asp Glu Ile Arg Lys Arg  
 20 25 30  
 Val Phe Glu Met Ala Asn Tyr Val Asn Met Leu Tyr Lys Lys Leu Asn  
 35 40 45  
 Thr His Val Ala Leu Val Gly Met Glu Ile Trp Thr Asp Lys Asp Lys  
 50 55 60

Ile	Lys	Ile	Thr	Pro	Asn	Ala	Ser	Phe	Thr	Leu	Glu	Asn	Phe	Ser	Lys
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Trp	Arg	Gly	Ser	Val	Leu	Ser	Arg	Arg	Lys	Arg	His	Asp	Ile	Ala	Gln
			85						90					95	
Leu	Ile	Thr	Ala	Thr	Glu	Leu	Ala	Gly	Thr	Thr	Val	Gly	Leu	Ala	Phe
			100					105					110		
Met	Ser	Thr	Met	Cys	Ser	Pro	Tyr	Ser	Val	Gly	Val	Val	Gln	Asp	His
		115					120					125			
Ser	Asp	Asn	Leu	Leu	Arg	Val	Ala	Gly	Thr	Met	Ala	His	Glu	Met	Gly
	130					135					140				
His	Asn	Phe	Gly	Met	Phe	His	Asp	Asp	Tyr	Ser	Cys	Lys	Cys	Pro	Ser
145					150					155					160
Thr	Ile	Cys	Val	Met	Asp	Lys	Ala	Leu	Ser	Phe	Tyr	Ile	Pro	Thr	Asp
				165					170					175	
Phe	Ser	Ser	Cys	Ser	Arg	Leu	Ser	Tyr	Asp	Lys	Phe	Phe	Glu	Asp	Lys
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<223> modified base

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<223> modified base

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ayytgwdbrd dwncdkvdds ngggca 26

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<223> Nucleic Acid primer

<400> 9  
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<400> 10  
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 <223> Nucleic Acid Primer  
  
 <400> 11  
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<210> 12  
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 <400> 12  
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<210> 13  
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<210> 14  
 <211> 29  
 <212> DNA  
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 <400> 14  
 aggactgtga ttgtgggacg tctgaggaa 29

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 <211> 775  
 <212> PRT  
 <213> Homo sapiens

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 <222> (1)..(775)  
 <223> An isolated ADAM family protein

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			20					25					30				
Pro	Ile	Arg	Leu	His	Pro	Leu	His	Lys	Arg	Glu	Ala	Lys	Glu	Pro	Glu		
		35					40					45					
Gln	Gln	Glu	Gln	Phe	Glu	Thr	Glu	Leu	Lys	Tyr	Lys	Met	Thr	Ile	Asn		
		50				55					60						
Gly	Lys	Ile	Ala	Val	Leu	Tyr	Leu	Lys	Lys	Asn	Lys	Asn	Leu	Leu	Ala		
65					70					75					80		
Pro	Gly	Tyr	Thr	Glu	Thr	Tyr	Tyr	Asn	Ser	Thr	Gly	Lys	Glu	Ile	Thr		
				85					90					95			
Thr	Ser	Pro	Gln	Ile	Met	Asp	Asp	Cys	Tyr	Tyr	Gln	Gly	His	Ile	Leu		
			100					105					110				
Asn	Glu	Lys	Val	Ser	Asp	Ala	Ser	Ile	Ser	Thr	Cys	Arg	Gly	Leu	Arg		
		115					120					125					
Gly	Tyr	Phe	Ser	Gln	Gly	Asp	Gln	Arg	Tyr	Phe	Ile	Glu	Pro	Leu	Ser		
	130					135					140						
Pro	Ile	His	Arg	Asp	Gly	Gln	Glu	His	Ala	Leu	Phe	Lys	Tyr	Asn	Pro		
145					150					155					160		
Asp	Glu	Lys	Asn	Tyr	Asp	Ser	Thr	Cys	Gly	Met	Asp	Gly	Val	Leu	Trp		
			165						170					175			
Ala	His	Asp	Leu	Gln	Gln	Asn	Ile	Ala	Leu	Pro	Ala	Thr	Lys	Leu	Val		
			180					185					190				
Lys	Leu	Lys	Asp	Arg	Lys	Val	Gln	Glu	His	Glu	Lys	Tyr	Ile	Glu	Tyr		
		195					200					205					
Tyr	Leu	Val	Leu	Asp	Asn	Gly	Glu	Phe	Lys	Arg	Tyr	Asn	Glu	Asn	Gln		
	210					215					220						
Asp	Glu	Ile	Arg	Lys	Arg	Val	Phe	Glu	Met	Ala	Asn	Tyr	Val	Asn	Met		
225					230					235					240		
Leu	Tyr	Lys	Lys	Leu	Asn	Thr	His	Val	Ala	Leu	Val	Gly	Met	Glu	Ile		
			245						250					255			
Trp	Thr	Asp	Lys	Asp	Lys	Ile	Lys	Ile	Thr	Pro	Asn	Ala	Ser	Phe	Thr		
		260						265					270				
Leu	Glu	Asn	Phe	Ser	Lys	Trp	Arg	Gly	Ser	Val	Leu	Ser	Arg	Arg	Lys		
		275					280					285					
Arg	His	Asp	Ile	Ala	Gln	Leu	Ile	Thr	Ala	Thr	Glu	Leu	Ala	Gly	Thr		
	290					295					300						
Thr	Val	Gly	Leu	Ala	Phe	Met	Ser	Thr	Met	Cys	Ser	Pro	Tyr	Ser	Val		
305					310					315					320		
Gly	Val	Val	Gln	Asp	His	Ser	Asp	Asn	Leu	Leu	Arg	Val	Ala	Gly	Thr		
			325						330					335			
Met	Ala	His	Glu	Met	Gly	His	Asn	Phe	Gly	Met	Phe	His	Asp	Asp	Tyr		
			340					345					350				
Ser	Cys	Lys	Cys	Pro	Ser	Thr	Ile	Cys	Val	Met	Asp	Lys	Ala	Leu	Ser		
		355					360					365					
Phe	Tyr	Ile	Pro	Thr	Asp	Phe	Ser	Ser	Cys	Ser	Arg	Leu	Ser	Tyr	Asp		
	370					375					380						
Lys	Phe	Phe	Glu	Asp	Lys	Leu	Ser	Asn	Cys	Leu	Phe	Asn	Ala	Pro	Leu		
385					390					395					400		
Pro	Thr	Asp	Ile	Ile	Ser	Thr	Pro	Ile	Cys	Gly	Asn	Gln	Leu	Val	Glu		
			405						410					415			
Met	Gly	Glu	Asp	Cys	Asp	Cys	Gly	Thr	Ser	Glu	Glu	Cys	Thr	Asn	Ile		
			420					425					430				
Cys	Cys	Asp	Ala	Lys	Thr	Cys	Lys	Ile	Lys	Ala	Thr	Phe	Gln	Cys	Ala		
		435					440					445					
Leu	Gly	Glu	Cys	Cys	Glu	Lys	Cys	Gln	Phe	Lys	Lys	Ala	Gly	Met	Val		
	450					455						460					

Cys Arg Pro Ala Lys Asp Glu Cys Asp Leu Pro Glu Met Cys Asn Gly  
 465 470 475 480  
 Lys Ser Gly Asn Cys Pro Asp Asp Arg Phe Gln Val Asn Gly Phe Pro  
 485 490 495  
 Cys His His Gly Lys Gly His Cys Leu Met Gly Thr Cys Pro Thr Leu  
 500 505 510  
 Gln Glu Gln Cys Thr Glu Leu Trp Gly Pro Gly Thr Glu Val Ala Asp  
 515 520 525  
 Lys Ser Cys Tyr Asn Arg Asn Glu Gly Gly Ser Lys Tyr Gly Tyr Cys  
 530 535 540  
 Arg Arg Val Asp Asp Thr Leu Ile Pro Cys Lys Ala Asn Asp Thr Met  
 545 550 555 560  
 Cys Gly Lys Leu Phe Cys Gln Gly Gly Ser Asp Asn Leu Pro Trp Lys  
 565 570 575  
 Gly Arg Ile Val Thr Phe Leu Thr Cys Lys Thr Phe Asp Pro Glu Asp  
 580 585 590  
 Thr Ser Gln Glu Ile Gly Met Val Ala Asn Gly Thr Lys Cys Gly Asp  
 595 600 605  
 Asn Lys Val Cys Ile Asn Ala Glu Cys Val Asp Ile Glu Lys Ala Tyr  
 610 615 620  
 Lys Ser Thr Asn Cys Ser Ser Lys Cys Lys Gly His Ala Val Cys Asp  
 625 630 635 640  
 His Glu Leu Gln Cys Gln Cys Glu Glu Gly Trp Ile Pro Pro Asp Cys  
 645 650 655  
 Asp Asp Ser Ser Val Val Phe His Phe Ser Ile Val Val Gly Val Leu  
 660 665 670  
 Phe Pro Met Ala Val Ile Phe Val Val Val Ala Met Val Ile Arg His  
 675 680 685  
 Gln Ser Ser Arg Glu Lys Gln Lys Lys Asp Gln Arg Pro Leu Ser Thr  
 690 695 700  
 Thr Gly Thr Arg Pro His Lys Gln Lys Arg Lys Pro Gln Met Val Lys  
 705 710 715 720  
 Ala Val Gln Pro Gln Glu Met Ser Gln Met Lys Pro His Val Tyr Asp  
 725 730 735  
 Leu Pro Val Glu Gly Asn Glu Pro Pro Ala Ser Phe His Lys Asp Thr  
 740 745 750  
 Asn Ala Leu Pro Pro Thr Val Phe Lys Asp Asn Pro Met Ser Thr Pro  
 755 760 765  
 Lys Asp Ser Asn Pro Lys Ala  
 770 775

<210> 16

<211> 2325

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)..(2325)

<223> Isolated nucleic acid encoding for a protein of SEQ ID NO. 15

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gaactccctg ggggtgaagaa gtatgaagtg gtttataccta taagacttca tccactgcac 120

aaaagagagg ccaaagagcc agagcaacag gaacaatttg aaactgaatt aaagtataaa	180
atgacaatta atggaaaaaat tgcagtgcctt tatttgaaaa aaaacaagaa cctccttgca	240
ccaggctaca cggaaacata ttataattcc actggaaagg agatcaccac aagcccacaa	300
attatggatg attgttatta tcaaggacat attcttaatg aaaaggtttc tgacgctagc	360
atcagcacat gtaggggtct aaggggctac ttcagtcagg gggatcaaag atactttatt	420
gaacctttta gccccatata tcgggatgga caggagcatg cactcttcaa gtataaccct	480
gatgaaaaga attatgacag cacctgtggg atggatgggtg tgttgtgggc ccacgatttg	540
cagcagaaca ttgccctacc tgccaccaa ctagtaaaat tgaaagacag gaaggttcag	600
gaacatgaga aatacataga atattatttg gtccctggata atgggtgagtt taaaaggtag	660
aatgagaatc aagatgagat cagaaagagg gtatttgaga tggctaatta tgtcaacatg	720
ctttataaaa agctcaatac tcatgtggcc ttagttggta tggaaatctg gactgacaag	780
gataagataa agataacccc aaatgcaagc ttcaccttgg agaatttttc taaatggagg	840
gggagtgttc tctcaagaag aaagcgcat gatattgctc agttaatcac agcaacagaa	900
cttgctggaa cgactgtggg tcttgcattt atgtctacaa tgtgttctcc ttattctgtt	960
ggcgttggtc aggaccacag cgataatctt ctagagttg cagggacaat ggcacatgaa	1020
atgggccaca actttggaat gtttcatgac gactattctt gcaagtgtcc ttctacaata	1080
tgtgtgatgg acaaagcact gagcttctat ataccacag acttcagttc ctgcagccgt	1140
ctcagctatg acaagttttt tgaagataaa ttatcaaatt gcctctttaa tgctccattg	1200
cctacagata tcatatccac tccaatttgt gggaaccagt tgggtggaaat gggagaggac	1260
tgtgattgtg ggacatctga ggaatgtacc aatatttgct gtgatgctaa gacatgtaaa	1320
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aagggccact gcttgatggg gacatgcccc aactgcagg agcagtgcac agagctgtgg	1560
ggaccaggaa ctgaggttgc agataagtca tgttacaaca ggaatgaagg tgggtcaaag	1620
tacgggtact gtcgcagagt ggatgacaca ctcatccct gcaaagcaaa tgataccatg	1680
tgtgggaagt tgttctgtca aggtgggtcg gataatttgc cctggaaagg acggatagtg	1740
actttcctga catgtaaaac atttgatcct gaagacacaa gtcaagaaat aggcattggtg	1800
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 ccactatcta ccactggcac caggccacac aaacagaaga ggaaacccca gatggtaaag 2160  
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 ggcaatgagc cccagcctc ttttcataaa gacacaaacg cacttcccc tactgttttc 2280  
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Leu Gln Gly Leu Leu Pro Val Ser Leu Leu Leu Ser Val Ala Val Ser  
5 10 15

gct ata aaa gaa ctc cct ggg gtg aag aag tat gaa gtg gtt tat cct 153  
Ala Ile Lys Glu Leu Pro Gly Val Lys Lys Tyr Glu Val Val Tyr Pro  
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ata aga ctt cat cca ctg cat aaa aga gag gcc aaa gag cca gag caa 201  
Ile Arg Leu His Pro Leu His Lys Arg Glu Ala Lys Glu Pro Glu Gln  
35 40 45

cag gaa caa ttt gaa act gaa tta aag tat aaa atg aca att aat gga 249  
Gln Glu Gln Phe Glu Thr Glu Leu Lys Tyr Lys Met Thr Ile Asn Gly  
50 55 60 65

aaa att gca gtg ctt tat ttg aaa aaa aac aag aac ctc ctt gca cca 297  
Lys Ile Ala Val Leu Tyr Leu Lys Lys Asn Lys Asn Leu Leu Ala Pro  
70 75 80

ggc tac acg gaa aca tat tat aat tcc act gga aag gag atc acc aca 345  
Gly Tyr Thr Glu Thr Tyr Tyr Asn Ser Thr Gly Lys Glu Ile Thr Thr  
85 90 95

agc cca caa att atg gat gat tgt tat tat caa gga cat att ctt aat 393  
Ser Pro Gln Ile Met Asp Asp Cys Tyr Tyr Gln Gly His Ile Leu Asn  
100 105 110

gaa aag gtt tct gac gct agc atc agc aca tgt agg ggt cta agg ggc 441  
Glu Lys Val Ser Asp Ala Ser Ile Ser Thr Cys Arg Gly Leu Arg Gly  
115 120 125

tac ttc agt cag ggg gat caa aga tac ttt att gaa cct tta agc ccc 489  
Tyr Phe Ser Gln Gly Asp Gln Arg Tyr Phe Ile Glu Pro Leu Ser Pro  
130 135 140 145

ata cat cgg gat gga cag gag cat gca ctc ttc aag tat aac cct gat 537  
Ile His Arg Asp Gly Gln Glu His Ala Leu Phe Lys Tyr Asn Pro Asp  
150 155 160

gaa aag aat tat gac agc acc tgt ggg atg gat ggt gtg ttg tgg gcc	585
Glu Lys Asn Tyr Asp Ser Thr Cys Gly Met Asp Gly Val Leu Trp Ala	
165 170 175	
cac gat ttg cag cag aac att gcc cta cct gcc acc aaa cta gta aaa	633
His Asp Leu Gln Gln Asn Ile Ala Leu Pro Ala Thr Lys Leu Val Lys	
180 185 190	
ttg aaa gac agg aag gtt cag gaa cat gag aaa tac ata gaa tat tat	681
Leu Lys Asp Arg Lys Val Gln Glu His Glu Lys Tyr Ile Glu Tyr Tyr	
195 200 205	
ttg gtc ctg gat aat ggt gag ttt aaa agg tac aat gag aat caa gat	729
Leu Val Leu Asp Asn Gly Glu Phe Lys Arg Tyr Asn Glu Asn Gln Asp	
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gag atc aga aag agg gta ttt gag atg gct aat tat gtc aac atg ctt	777
Glu Ile Arg Lys Arg Val Phe Glu Met Ala Asn Tyr Val Asn Met Leu	
230 235 240	
tat aaa aag ctc aat act cat gtg gcc tta gtt ggt atg gaa atc tgg	825
Tyr Lys Lys Leu Asn Thr His Val Ala Leu Val Gly Met Glu Ile Trp	
245 250 255	
act gac aag gat aag ata aag ata acc cca aat gca agc ttc acc ttg	873
Thr Asp Lys Asp Lys Ile Lys Ile Thr Pro Asn Ala Ser Phe Thr Leu	
260 265 270	
gag aat ttt tct aaa tgg agg ggg agt gtt ctc tca aga aga aag cgt	921
Glu Asn Phe Ser Lys Trp Arg Gly Ser Val Leu Ser Arg Arg Lys Arg	
275 280 285	
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His Asp Ile Ala Gln Leu Ile Thr Ala Thr Glu Leu Ala Gly Thr Thr	
290 295 300 305	
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Val Gly Leu Ala Phe Met Ser Thr Met Cys Ser Pro Tyr Ser Val Gly	
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Val Val Gln Asp His Ser Asp Asn Leu Leu Arg Val Ala Gly Thr Met	
325 330 335	
gca cat gaa atg ggc cac aac ttt gga atg ttt cat gac gac tat tct	1113
Ala His Glu Met Gly His Asn Phe Gly Met Phe His Asp Asp Tyr Ser	
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tgc aag tgt cct tct aca ata tgt gtg atg gac aaa gca ctg agc ttc	1161
Cys Lys Cys Pro Ser Thr Ile Cys Val Met Asp Lys Ala Leu Ser Phe	
355 360 365	
tat ata ccc aca gac ttc agt tcc tgc agc cgt ctc agc tat gac aag	1209
Tyr Ile Pro Thr Asp Phe Ser Ser Cys Ser Arg Leu Ser Tyr Asp Lys	
370 375 380 385	



ttt ttt gaa gat aaa tta tca aat tgc ctc ttt aat gct cca ttg cct	1257
Phe Phe Glu Asp Lys Leu Ser Asn Cys Leu Phe Asn Ala Pro Leu Pro	
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aca gat atc ata tcc act cca att tgt ggg aac cag ttg gtg gaa atg	1305
Thr Asp Ile Ile Ser Thr Pro Ile Cys Gly Asn Gln Leu Val Glu Met	
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gga gag gac tgt gat tgt ggg aca tct gag gaa tgt acc aat att tgc	1353
Gly Glu Asp Cys Asp Cys Gly Thr Ser Glu Glu Cys Thr Asn Ile Cys	
420 425 430	
tgt gat gct aag aca tgt aaa atc aaa gca act ttt caa tgt gca tta	1401
Cys Asp Ala Lys Thr Cys Lys Ile Lys Ala Thr Phe Gln Cys Ala Leu	
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Gly Glu Cys Cys Glu Lys Cys Gln Phe Lys Lys Ala Gly Met Val Cys	
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Arg Pro Ala Lys Asp Glu Cys Asp Leu Pro Glu Met Cys Asn Gly Lys	
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Ser Gly Asn Cys Pro Asp Asp Arg Phe Gln Val Asn Gly Phe Pro Cys	
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His His Gly Lys Gly His Cys Leu Met Gly Thr Cys Pro Thr Leu Gln	
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Glu Gln Cys Thr Glu Leu Trp Gly Pro Gly Arg Arg Thr Asn Pro Phe	
515 520 525	
ccc tgt gca tgt gcg aag gaa aat cat ttc aga tgacagtgtt taaccatggt	1694
Pro Cys Ala Cys Ala Lys Glu Asn His Phe Arg	
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cgttaaatth taacttaaaa ttaacaagtt ttttgtaaatt tttttgtttt ttgtctcagc	1874
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in of SEQ ID NO:1  
  
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35 40 45

Gln Gln Glu Gln Phe Glu Thr Glu Leu Lys Tyr Lys Met Thr Ile Asn  
50 55 60

Gly Lys Ile Ala Val Leu Tyr Leu Lys Lys Asn Lys Asn Leu Leu Ala  
65 70 75 80

Pro Gly Tyr Thr Glu Thr Tyr Tyr Asn Ser Thr Gly Lys Glu Ile Thr  
85 90 95

Thr Ser Pro Gln Ile Met Asp Asp Cys Tyr Tyr Gln Gly His Ile Leu  
100 105 110

Asn Glu Lys Val Ser Asp Ala Ser Ile Ser Thr Cys Arg Gly Leu Arg  
115 120 125

Gly Tyr Phe Ser Gln Gly Asp Gln Arg Tyr Phe Ile Glu Pro Leu Ser  
 130 135 140

Pro Ile His Arg Asp Gly Gln Glu His Ala Leu Phe Lys Tyr Asn Pro  
 145 150 155 160

Asp Glu Lys Asn Tyr Asp Ser Thr Cys Gly Met Asp Gly Val Leu Trp  
 165 170 175

Ala His Asp Leu Gln Gln Asn Ile Ala Leu Pro Ala Thr Lys Leu Val  
 180 185 190

Lys Leu Lys Asp Arg Lys Val Gln Glu His Glu Lys Tyr Ile Glu Tyr  
 195 200 205

Tyr Leu Val Leu Asp Asn Gly Glu Phe Lys Arg Tyr Asn Glu Asn Gln  
 210 215 220

Asp Glu Ile Arg Lys Arg Val Phe Glu Met Ala Asn Tyr Val Asn Met  
 225 230 235 240

Leu Tyr Lys Lys Leu Asn Thr His Val Ala Leu Val Gly Met Glu Ile  
 245 250 255

Trp Thr Asp Lys Asp Lys Ile Lys Ile Thr Pro Asn Ala Ser Phe Thr  
 260 265 270

Leu Glu Asn Phe Ser Lys Trp Arg Gly Ser Val Leu Ser Arg Arg Lys  
 275 280 285

Arg His Asp Ile Ala Gln Leu Ile Thr Ala Thr Glu Leu Ala Gly Thr  
 290 295 300

Thr Val Gly Leu Ala Phe Met Ser Thr Met Cys Ser Pro Tyr Ser Val  
 305 310 315 320

Gly Val Val Gln Asp His Ser Asp Asn Leu Leu Arg Val Ala Gly Thr  
 325 330 335

Met Ala His Glu Met Gly His Asn Phe Gly Met Phe His Asp Asp Tyr  
 340 345 350

Ser Cys Lys Cys Pro Ser Thr Ile Cys Val Met Asp Lys Ala Leu Ser  
 355 360 365

Phe Tyr Ile Pro Thr Asp Phe Ser Ser Cys Ser Arg Leu Ser Tyr Asp  
 370 375 380

Lys Phe Phe Glu Asp Lys Leu Ser Asn Cys Leu Phe Asn Ala Pro Leu  
 385 390 395 400

Pro Thr Asp Ile Ile Ser Thr Pro Ile Cys Gly Asn Gln Leu Val Glu  
 405 410 415

Met Gly Glu Asp Cys Asp Cys Gly Thr Ser Glu Glu Cys Thr Asn Ile  
 420 425 430

Cys Cys Asp Ala Lys Thr Cys Lys Ile Lys Ala Thr Phe Gln Cys Ala  
 435 440 445

Leu Gly Glu Cys Cys Glu Lys Cys Gln Phe Lys Lys Ala Gly Met Val  
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Cys Arg Pro Ala Lys Asp Glu Cys Asp Leu Pro Glu Met Cys Asn Gly  
 465 470 475 480

Lys Ser Gly Asn Cys Pro Asp Asp Arg Phe Gln Val Asn Gly Phe Pro  
 485 490 495

Cys His His Gly Lys Gly His Cys Leu Met Gly Thr Cys Pro Thr Leu  
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His Asp Leu Gln Gln Asn Ile Ala Leu Pro Ala Thr Lys Leu Val Lys	
180 185 190	
ttg aaa gac agg aag gtt cag gaa cat gag aaa tac ata gaa tat tat	681
Leu Lys Asp Arg Lys Val Gln Glu His Glu Lys Tyr Ile Glu Tyr Tyr	
195 200 205	
ttg gtc ctg gat aat ggt gag ttt aaa agg tac aat gag aat caa gat	729
Leu Val Leu Asp Asn Gly Glu Phe Lys Arg Tyr Asn Glu Asn Gln Asp	
210 215 220 225	
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Glu Ile Arg Lys Arg Val Phe Glu Met Ala Asn Tyr Val Asn Met Leu	
230 235 240	
tat aaa aag ctc aat act cat gtg gcc tta gtt ggt atg gaa atc tgg	825
Tyr Lys Lys Leu Asn Thr His Val Ala Leu Val Gly Met Glu Ile Trp	
245 250 255	
act gac aag gat aag ata aag ata acc cca aat gca agc ttc acc ttg	873
Thr Asp Lys Asp Lys Ile Lys Ile Thr Pro Asn Ala Ser Phe Thr Leu	
260 265 270	
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Glu Asn Phe Ser Lys Trp Arg Gly Ser Val Leu Ser Arg Arg Lys Arg	
275 280 285	
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Val Val Gln Asp His Ser Asp Asn Leu Leu Arg Val Ala Gly Thr Met	
325 330 335	
gca cat gaa atg ggc cac aac ttt gga atg ttt cat gac gac tat tct	1113
Ala His Glu Met Gly His Asn Phe Gly Met Phe His Asp Asp Tyr Ser	
340 345 350	
tgc aag tgt cct tct aca ata tgt gtg atg gac aaa gca ctg agc ttc	1161
Cys Lys Cys Pro Ser Thr Ile Cys Val Met Asp Lys Ala Leu Ser Phe	
355 360 365	
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Tyr Ile Pro Thr Asp Phe Ser Ser Cys Ser Arg Leu Ser Tyr Asp Lys	
370 375 380 385	
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Phe	Phe	Glu	Asp	Lys	Leu	Ser	Asn	Cys	Leu	Phe	Asn	Ala	Pro	Leu	Pro	
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Thr	Asp	Ile	Ile	Ser	Thr	Pro	Ile	Cys	Gly	Asn	Gln	Leu	Val	Glu	Met	
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Gly	Glu	Asp	Cys	Asp	Cys	Gly	Thr	Ser	Glu	Glu	Cys	Thr	Asn	Ile	Cys	
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tgt	gat	gct	aag	aca	tgt	aaa	atc	aaa	gca	act	ttt	caa	tgt	gca	tta	1401
Cys	Asp	Ala	Lys	Thr	Cys	Lys	Ile	Lys	Ala	Thr	Phe	Gln	Cys	Ala	Leu	
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gga	gaa	tgt	tgt	gaa	aaa	tgc	caa	ttt	aaa	aag	gct	ggg	atg	gtg	tgc	1449
Gly	Glu	Cys	Cys	Glu	Lys	Cys	Gln	Phe	Lys	Lys	Ala	Gly	Met	Val	Cys	
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Arg	Pro	Ala	Lys	Asp	Glu	Cys	Asp	Leu	Pro	Glu	Met	Cys	Asn	Gly	Lys	
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tct	ggg	aat	tgt	cct	gat	gat	aga	ttc	caa	gtc	aat	ggc	ttc	cct	tgc	1545
Ser	Gly	Asn	Cys	Pro	Asp	Asp	Arg	Phe	Gln	Val	Asn	Gly	Phe	Pro	Cys	
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cat	cac	ggg	aag	ggc	cac	tgc	ttg	atg	ggg	aca	tgc	ccc	aca	ctg	cag	1593
His	His	Gly	Lys	Gly	His	Cys	Leu	Met	Gly	Thr	Cys	Pro	Thr	Leu	Gln	
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Glu	Gln	Cys	Thr	Glu	Leu	Trp	Gly	Pro	Gly	Thr	Glu	Val	Ala	Asp	Lys	
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tca	tgt	tac	aac	agg	aat	gaa	ggg	ggg	tca	aag	tac	ggg	tac	tgt	cgc	1689
Ser	Cys	Tyr	Asn	Arg	Asn	Glu	Gly	Gly	Ser	Lys	Tyr	Gly	Tyr	Cys	Arg	
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Gly	Lys	Leu	Phe	Cys	Gln	Gly	Gly	Ser	Asp	Asn	Leu	Pro	Trp	Lys	Gly	
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cgg	ata	gtg	act	ttc	ctg	aca	tgt	aaa	aca	ttt	gat	cct	gaa	gac	aca	1833
Arg	Ile	Val	Thr	Phe	Leu	Thr	Cys	Lys	Thr	Phe	Asp	Pro	Glu	Asp	Thr	
		580					585					590				
agt	caa	gaa	ata	ggc	atg	gtg	gcc	aat	gga	act	aag	tgt	ggc	gat	aac	1881
Ser	Gln	Glu	Ile	Gly	Met	Val	Ala	Asn	Gly	Thr	Lys	Cys	Gly	Asp	Asn	
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aag	gtt	tgc	att	aat	gca	gaa	tgt	gtg	gat	att	gag	aaa	gcc	tac	aaa	1929
Lys	Val	Cys	Ile	Asn	Ala	Glu	Cys	Val	Asp	Ile	Glu	Lys	Ala	Tyr	Lys	

610	615	620	625	
tca acc aat tgc tca tct aag tgc aaa gga cat gct gtg tgt gac cat				1977
Ser Thr Asn Cys Ser Ser Lys Cys Lys Gly His Ala Val Cys Asp His	630	635	640	
gag ctc cag tgt caa tgt gag gaa gga tgg atc cct ccc gac tgc gat				2025
Glu Leu Gln Cys Gln Cys Glu Glu Gly Trp Ile Pro Pro Asp Cys Asp	645	650	655	
gac tcc tca gtg gtc ttc cac ttc tcc att gtg gtt ggg gtg ctg ttc				2073
Asp Ser Ser Val Val Phe His Phe Ser Ile Val Val Gly Val Leu Phe	660	665	670	
cca atg gcg gtc att ttt gtg gtg gtt gct atg gta atc cgg cac cag				2121
Pro Met Ala Val Ile Phe Val Val Val Ala Met Val Ile Arg His Gln	675	680	685	
agc tcc aga gaa aag cag aag aaa gat cag agg cca cta tct acc act				2169
Ser Ser Arg Glu Lys Gln Lys Lys Asp Gln Arg Pro Leu Ser Thr Thr	690	695	700	705
ggc acc agg cca cac aaa cag aag agg aaa ccc cag atg gta aag gct				2217
Gly Thr Arg Pro His Lys Gln Lys Arg Lys Pro Gln Met Val Lys Ala	710	715	720	
gtt caa ccc caa gag atg agt cag atg aag ccc cat gtg tat gat ctg				2265
Val Gln Pro Gln Glu Met Ser Gln Met Lys Pro His Val Tyr Asp Leu	725	730	735	
cca gta gaa ggc aat gag ccc cca gcc tct ttt cat aaa gac aca aac				2313
Pro Val Glu Gly Asn Glu Pro Pro Ala Ser Phe His Lys Asp Thr Asn	740	745	750	
gca ctt ccc cct act gtt ttc aag gat aat cca atg tct aca cct aag				2361
Ala Leu Pro Pro Thr Val Phe Lys Asp Asn Pro Met Ser Thr Pro Lys	755	760	765	
gac tca aat cca aaa gca tgaagcaaca gctaagcaag aactaatggc				2409
Asp Ser Asn Pro Lys Ala	770	775		
taaattatca acttggaaaa ctggaaaatc tggatggcag agaaatatac tatctcacca				2469
gtatttgctc tcgactcaag aaggttaaca ttttctgatt catgttagac tttgaagaga				2529
ctaaagaaaa ttttcaagag gaacatatgc ctgagaacct ttgcatgaat ttaaaatttc				2589
aattatccat tcttataaga aggaagatga ttgtaaagaa atatctccga agttaaaatc				2649
tgtaatagga attgattcat tctctaataa aaacaaaaca taaaaacatc acactaatct				2709
tggaggaata agaaaaattg tacatccatt aaatgtacaa ttgattgcaa catcttgatt				2769
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Pro Ile Arg Leu His Pro Leu His Lys Arg Glu Ala Lys Glu Pro Glu  
 35 40 45

Gln Gln Glu Gln Phe Glu Thr Glu Leu Lys Tyr Lys Met Thr Ile Asn  
 50 55 60

Gly Lys Ile Ala Val Leu Tyr Leu Lys Lys Asn Lys Asn Leu Leu Ala  
 65 70 75 80

Pro Gly Tyr Thr Glu Thr Tyr Tyr Asn Ser Thr Gly Lys Glu Ile Thr  
 85 90 95

Thr Ser Pro Gln Ile Met Asp Asp Cys Tyr Tyr Gln Gly His Ile Leu  
 100 105 110

Asn Glu Lys Val Ser Asp Ala Ser Ile Ser Thr Cys Arg Gly Leu Arg  
 115 120 125

Gly Tyr Phe Ser Gln Gly Asp Gln Arg Tyr Phe Ile Glu Pro Leu Ser  
 130 135 140

Pro Ile His Arg Asp Gly Gln Glu His Ala Leu Phe Lys Tyr Asn Pro  
 145 150 155 160

Asp Glu Lys Asn Tyr Asp Ser Thr Cys Gly Met Asp Gly Val Leu Trp  
 165 170 175

Ala His Asp Leu Gln Gln Asn Ile Ala Leu Pro Ala Thr Lys Leu Val  
 180 185 190

Lys Leu Lys Asp Arg Lys Val Gln Glu His Glu Lys Tyr Ile Glu Tyr  
 195 200 205

Tyr Leu Val Leu Asp Asn Gly Glu Phe Lys Arg Tyr Asn Glu Asn Gln  
 210 215 220

Asp Glu Ile Arg Lys Arg Val Phe Glu Met Ala Asn Tyr Val Asn Met  
 225 230 235 240

Leu Tyr Lys Lys Leu Asn Thr His Val Ala Leu Val Gly Met Glu Ile  
 245 250 255

Trp Thr Asp Lys Asp Lys Ile Lys Ile Thr Pro Asn Ala Ser Phe Thr  
 260 265 270

Leu Glu Asn Phe Ser Lys Trp Arg Gly Ser Val Leu Ser Arg Arg Lys  
 275 280 285

Arg His Asp Ile Ala Gln Leu Ile Thr Ala Thr Glu Leu Ala Gly Thr  
 290 295 300

Thr Val Gly Leu Ala Phe Met Ser Thr Met Cys Ser Pro Tyr Ser Val  
 305 310 315 320

Gly Val Val Gln Asp His Ser Asp Asn Leu Leu Arg Val Ala Gly Thr  
 325 330 335

Met Ala His Glu Met Gly His Asn Phe Gly Met Phe His Asp Asp Tyr  
 340 345 350

Ser Cys Lys Cys Pro Ser Thr Ile Cys Val Met Asp Lys Ala Leu Ser  
 355 360 365

Phe Tyr Ile Pro Thr Asp Phe Ser Ser Cys Ser Arg Leu Ser Tyr Asp  
 370 375 380

Lys Phe Phe Glu Asp Lys Leu Ser Asn Cys Leu Phe Asn Ala Pro Leu  
 385 390 395 400

Pro Thr Asp Ile Ile Ser Thr Pro Ile Cys Gly Asn Gln Leu Val Glu

405								410				415			
Met	Gly	Glu	Asp	Cys	Asp	Cys	Gly	Thr	Ser	Glu	Glu	Cys	Thr	Asn	Ile
			420											430	
Cys	Cys	Asp	Ala	Lys	Thr	Cys	Lys	Ile	Lys	Ala	Thr	Phe	Gln	Cys	Ala
		435					440						445		
Leu	Gly	Glu	Cys	Cys	Glu	Lys	Cys	Gln	Phe	Lys	Lys	Ala	Gly	Met	Val
	450					455					460				
Cys	Arg	Pro	Ala	Lys	Asp	Glu	Cys	Asp	Leu	Pro	Glu	Met	Cys	Asn	Gly
465					470					475					480
Lys	Ser	Gly	Asn	Cys	Pro	Asp	Asp	Arg	Phe	Gln	Val	Asn	Gly	Phe	Pro
			485						490					495	
Cys	His	His	Gly	Lys	Gly	His	Cys	Leu	Met	Gly	Thr	Cys	Pro	Thr	Leu
			500				505						510		
Gln	Glu	Gln	Cys	Thr	Glu	Leu	Trp	Gly	Pro	Gly	Thr	Glu	Val	Ala	Asp
		515					520					525			
Lys	Ser	Cys	Tyr	Asn	Arg	Asn	Glu	Gly	Gly	Ser	Lys	Tyr	Gly	Tyr	Cys
	530					535					540				
Arg	Arg	Val	Asp	Asp	Thr	Leu	Ile	Pro	Cys	Lys	Ala	Asn	Asp	Thr	Met
545					550					555					560
Cys	Gly	Lys	Leu	Phe	Cys	Gln	Gly	Gly	Ser	Asp	Asn	Leu	Pro	Trp	Lys
				565					570					575	
Gly	Arg	Ile	Val	Thr	Phe	Leu	Thr	Cys	Lys	Thr	Phe	Asp	Pro	Glu	Asp
			580						585				590		
Thr	Ser	Gln	Glu	Ile	Gly	Met	Val	Ala	Asn	Gly	Thr	Lys	Cys	Gly	Asp
		595					600					605			
Asn	Lys	Val	Cys	Ile	Asn	Ala	Glu	Cys	Val	Asp	Ile	Glu	Lys	Ala	Tyr
	610					615					620				
Lys	Ser	Thr	Asn	Cys	Ser	Ser	Lys	Cys	Lys	Gly	His	Ala	Val	Cys	Asp
625					630					635					640

His Glu Leu Gln Cys Gln Cys Glu Glu Gly Trp Ile Pro Pro Asp Cys  
645 650 655

Asp Asp Ser Ser Val Val Phe His Phe Ser Ile Val Val Gly Val Leu  
660 665 670

Phe Pro Met Ala Val Ile Phe Val Val Val Ala Met Val Ile Arg His  
675 680 685

Gln Ser Ser Arg Glu Lys Gln Lys Lys Asp Gln Arg Pro Leu Ser Thr  
690 695 700

Thr Gly Thr Arg Pro His Lys Gln Lys Arg Lys Pro Gln Met Val Lys  
705 710 715 720

Ala Val Gln Pro Gln Glu Met Ser Gln Met Lys Pro His Val Tyr Asp  
725 730 735

Leu Pro Val Glu Gly Asn Glu Pro Pro Ala Ser Phe His Lys Asp Thr  
740 745 750

Asn Ala Leu Pro Pro Thr Val Phe Lys Asp Asn Pro Met Ser Thr Pro  
755 760 765

Lys Asp Ser Asn Pro Lys Ala  
770 775